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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: Tue Sep 04 14:58:00 EDT 2007

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Application No: 10573658

Version No: 1.0

Input Set:**Output Set:****Started:** 2007-08-20 10:49:56.980**Finished:** 2007-08-20 10:49:59.210**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 230 ms**Total Warnings:** 59**Total Errors:** 32**No. of SeqIDs Defined:** 59**Actual SeqID Count:** 59

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
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W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
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W 213	Artificial or Unknown found in <213> in SEQ ID (14)
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W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set :

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Started:      2007-08-20 10:49:56.980
Finished:    2007-08-20 10:49:59.210
Elapsed:     0 hr(s) 0 min(s) 2 sec(s) 230 ms
Total Warnings: 59
Total Errors:  32
No. of SeqIDs Defined: 59
Actual SeqID Count: 59

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Error code	Error Description
E 336	This error has occurred more than 20 times, will not be displayed Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
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SEQUENCE LISTING

<110> MCKERRACHER, LISA
LASKO, DANA

<120> CLOSTRIDIUM BOTULINUM C3 EXOTRANSFERASE COMPOSITIONS AND METHODS
FOR TREATING TUMOUR SPREADING

<130> 1912-0330PUS1

<140> 10573658

<141> 2007-08-20

<150> PCT/CA04/01763

<151> 2004-09-29

<150> US 10/902,879

<151> 2004-08-02

<150> US 60/506,162

<151> 2003-09-29

<160> 59

<170> PatentIn version 3.1

<210> 1

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide used to remove the stop codon from ADP-ribosyl
transferase C3 (Clostridium botulinum) cDNA.

<400> 1

gaattcttta ggattgatag ctgtgcc

27

<210> 2

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used to remove the stop codon from ADP-ribosyl
transferase C3 (Clostridium botulinum) cDNA.

<400> 2

ggtggcgacc atcctcaaaa a

21

<210> 3

<211> 888

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3APL: includes ADP-ribosyl transferase C3
(Clostridium botulinum) and Antennapedia sequence.

<220>

<221> CDS

<222> (1)..(888)

<400> 3

gga tcc tct aga gtc gac ctg cag gca tgc aat gct tat tcc att aat	48
Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn	
1 5 10 15	

caa aag gct tat tca aat act tac cag gag ttt act aat att gat caa	96
Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln	
20 25 30	

gca aaa gct tgg ggt aat gct cag tat aaa aag tat gga cta agc aaa	144
Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys	
35 40 45	

tca gaa aaa gaa gct ata gta tca tat act aaa agc gct agt gaa ata	192
Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile	
50 55 60	

aat gga aag cta aga caa aat aag gga gtt atc aat gga ttt cct tca	240
Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser	
65 70 75 80	

aat tta ata aaa caa gtt gaa ctt tta gat aaa tct ttt aat aaa atg	288
Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met	
85 90 95	

aag acc cct gaa aat att atg tta ttt aga ggc gac gac cct gct tat	336
Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr	
100 105 110	

tta gga aca gaa ttt caa aac act ctt ctt aat tca aat ggt aca att	384
Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile	
115 120 125	

aat aaa acg gct ttt gaa aag gct aaa gct aag ttt tta aat aaa gat	432
Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp	
130 135 140	

aga ctt gaa tat gga tat att agt act tca tta atg aat gtc tct caa	480
Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln	
145 150 155 160	

ttt gca gga aga cca att att aca caa ttt aaa gta gca aaa ggc tca	528
Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser	
165 170 175	

aag gca gga tat att gac cct att agt gct ttt cag gga caa ctt gaa	576
Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu	

180	185	190	
atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg			624
Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu			
195	200	205	
tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca			672
Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr			
210	215	220	
gct atc aat cct aaa gaa ttc gtg atg gaa tcc cgc aaa cgc gca agg			720
Ala Ile Asn Pro Lys Glu Phe Val Met Glu Ser Arg Lys Arg Ala Arg			
225	230	235	240
cag aca tac acc cgg tac cag act cta gag cta gag aag gag ttt cac			768
Gln Thr Tyr Thr Arg Tyr Gln Thr Leu Glu Leu Glu Lys Glu Phe His			
245	250	255	
ttc aat cgc tac ttg acc cgt cgg cga agg atc gag atc gcc cac gcc			816
Phe Asn Arg Tyr Leu Thr Arg Arg Arg Arg Ile Glu Ile Ala His Ala			
260	265	270	
ctg tgc ctc acg gag cgc cag ata aag att tgg ttc cag aat cgg cgc			864
Leu Cys Leu Thr Glu Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg			
275	280	285	
atg aag tgg aag aag gag aac tga			888
Met Lys Trp Lys Lys Glu Asn			
290	295		

<210> 4

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3APLT: includes ADP-ribosyl transferase C3
(Clostridium botulinum) and Antennapedia sequence.

<400> 4

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn
1 5 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys
35 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser			
65	70	75	80
Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met			
	85	90	95
Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr			
	100	105	110
Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile			
	115	120	125
Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp			
	130	135	140
Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln			
	145	150	155
			160
Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser			
	165	170	175
Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu			
	180	185	190
Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu			
	195	200	205
Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr			
	210	215	220
Ala Ile Asn Pro Lys Glu Phe Val Met Glu Ser Arg Lys Arg Ala Arg			
	225	230	235
			240
Gln Thr Tyr Thr Arg Tyr Gln Thr Leu Glu Leu Glu Lys Glu Phe His			
	245	250	255
Phe Asn Arg Tyr Leu Thr Arg Arg Arg Arg Ile Glu Ile Ala His Ala			
	260	265	270
Leu Cys Leu Thr Glu Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg			
	275	280	285

Met Lys Trp Lys Lys Glu Asn
290 295

<210> 5

<211> 774

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence of C3APS: Includes ADP-ribosyl transferase C3
(Clostridium botulinum) and Antennapedia sequence.

<220>

<221> CDS

<222> (1)..(774)

<400> 5

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Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn
1 5 10 15

caa aag gct tat tca aat act tac cag gag ttt act aat att gat caa 96
Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

gca aaa gct tgg ggt aat gct cag tat aaa aag tat gga cta agc aaa 144
Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys
35 40 45

tca gaa aaa gaa gct ata gta tca tat act aaa agc gct agt gaa ata 192
Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

aat gga aag cta aga caa aat aag gga gtt atc aat gga ttt cct tca 240
Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser
65 70 75 80

aat tta ata aaa caa gtt gaa ctt tta gat aaa tct ttt aat aaa atg 288
Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met
85 90 95

aag acc cct gaa aat att atg tta ttt aga ggc gac gac cct gct tat 336
Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr
100 105 110

tta gga aca gaa ttt caa aac act ctt ctt aat tca aat ggt aca att 384
Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

aat aaa acg gct ttt gaa aag gct aaa gct aag ttt tta aat aaa gat 432
Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp
130 135 140

aga ctt gaa tat gga tat att agt act tca tta atg aat gtc tct caa 480
Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln

145	150	155	160	
ttt gca gga aga cca att att aca caa ttt aaa gta gca aaa ggc tca				528
Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser				
	165	170	175	
aag gca gga tat att gac cct att agt gct ttt cag gga caa ctt gaa				576
Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu				
	180	185	190	
atg ttg ctt cct aga cat agt act tat cat ata gac gat atg aga ttg				624
Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu				
	195	200	205	
tct tct gat ggt aaa caa ata ata att aca gca aca atg atg ggc aca				672
Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr				
	210	215	220	
gct atc aat cct aaa gaa ttc cgc cag atc aag att tgg ttc cag aat				720
Ala Ile Asn Pro Lys Glu Phe Arg Gln Ile Lys Ile Trp Phe Gln Asn				
	225	230	235	240
cgt cgc atg aag tgg aag aag gtc gac tcg agc ggc cgc atc gtg act				768
Arg Arg Met Lys Trp Lys Lys Val Asp Ser Ser Gly Arg Ile Val Thr				
	245	250	255	
gac tga				774
Asp				

<210> 6

<211> 257

<212> PRT

<213> Artificial Sequence

<220>

<223> Sequence of C3APS: Includes ADP-ribosyl transferase C3
(Clostridium botulinum) and Antennapedia sequence.

<400> 6

Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn
1 5 10 15

Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30

Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys
35 40 45

Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60

Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser
65 70 75 80

Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met
85 90 95

Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr
100 105 110

Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile
115 120 125

Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp
130 135 140

Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln
145 150 155 160

Phe Ala Gly Arg Pro Ile Ile Thr Gln Phe Lys Val Ala Lys Gly Ser
165 170 175

Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Gln Gly Gln Leu Glu
180 185 190

Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu
195 200 205

Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr
210 215 220

Ala Ile Asn Pro Lys Glu Phe Arg Gln Ile Lys Ile Trp Phe Gln Asn
225 230 235 240

Arg Arg Met Lys Trp Lys Lys Val Asp Ser Ser Gly Arg Ile Val Thr
245 250 255

Asp

<210> 7
<211> 24
<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the amplification of Antennapedia sequence

<400> 7
gaatcccgca aacgcgcaag gcag 24

<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the amplification of Antennapedia sequence

<400> 8
tcagttctcc ttcttccact tcatgcg 27

<210> 9
<211> 54
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of sequences from Antennapedia

<400> 9
aattccgccca gatcaagatt tggttccaga atcgtcgcat gaagtggaag aagg 54

<210> 10
<211> 54
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the cloning of sequences from Antennapedia

<400> 10
ggcgggtctag ttctaaacca agctcttagc agcgtagttc accttcttcc agct 54

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide used in the amplification of a sequence corresponding to amino acid 27-72 of HIV-1 Tat

<400> 11
gaatccaagc atccaggaag tcagcc 26

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide used in the amplification of a sequence
corresponding to amino acid 27-72 of HIV-1 Tat

<400> 12
accagccacc accttctgat a 21

<210> 13
<211> 876
<212> DNA
<213> Artificial Sequence

<220>
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(Clostridium botulinum) and HIV-1 Tat sequence.

<220>
<221> CDS
<222> (1)..(876)

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Gly Ser Ser Arg Val Asp Leu Gln Ala Cys Asn Ala Tyr Ser Ile Asn
1 5 10 15
caa aag gct tat tca aat act tac cag gag ttt act aat att gat caa 96
Gln Lys Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln
20 25 30
gca aaa gct tgg ggt aat gct cag tat aaa aag tat gga cta agc aaa 144
Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys
35 40 45
tca gaa aaa gaa gct ata gta tca tat act aaa agc gct agt gaa ata 192
Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile
50 55 60
aat gga aag cta aga caa aat aag gga gtt atc aat gga ttt cct tca 240
Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser
65 70 75 80
aat tta ata aaa caa gtt gaa ctt tta gat aaa tct ttt aat aaa atg 288
Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met